



SEQUENCE LISTING

<110> Ozezu, Jun-Ichi
Oku, Asuka

<120> TRANSPORTER GENES

<130> 06501-057001

<140> 09/521,195

<141> 2000-03-07

<150> JP 10/156660

<151> 1998-05-20

<150> JP 9/260972

<151> 1997-09-08

<150> PCT/JP98/04009

<151> 1998-09-07

<160> 32

<210> 1

<211> 551

<212> PRT

<213> Homo sapiens

<400> 1

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Phe	Gln	Arg	Leu	Ile	Phe	Phe	Leu	Leu	Ser	Ala	Ser	Ile	Ile	Pro	Asn
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Gly	Phe	Asn	Gly	Met	Ser	Val	Val	Phe	Leu	Ala	Gly	Thr	Pro	Glu	His
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Arg	Cys	Arg	Val	Pro	Asp	Ala	Asn	Leu	Ser	Ser	Ala	Trp	Arg	Asn	
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Asn	Ser	Val	Pro	Leu	Arg	Leu	Arg	Asp	Gly	Arg	Glu	Val	Pro	His	Ser
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Cys	Ser	Arg	Tyr	Arg	Leu	Ala	Thr	Ile	Ala	Asn	Phe	Ser	Ala	Leu	Gly
				85					90					95	
Leu	Glu	Pro	Gly	Arg	Asp	Val	Asp	Leu	Gly	Gln	Leu	Glu	Gln	Glu	Ser
			100						105					110	
Cys	Leu	Asp	Gly	Trp	Glu	Phe	Ser	Gln	Asp	Val	Tyr	Leu	Ser	Thr	Val
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Val	Thr	Glu	Trp	Asn	Leu	Val	Cys	Glu	Asp	Asn	Trp	Lys	Val	Pro	Leu
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Thr	Thr	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Leu	Gly	Ser	Phe	Val	Ser
145					150					155					160
Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Asn	Val	Leu	Phe	Ala	Thr
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Met	Ala	Val	Gln	Thr	Gly	Phe	Ser	Phe	Leu	Gln	Ile	Phe	Ser	Ile	Ser
			180						185					190	
Trp	Glu	Met	Phe	Thr	Val	Leu	Phe	Val	Ile	Val	Gly	Met	Gly	Gln	Ile
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Ser	Asn	Tyr	Val	Val	Ala	Phe	Ile	Leu	Gly	Thr	Glu	Ile	Leu	Gly	Lys
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Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
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 Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 Arg Met Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro
 260 265 270
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285
 Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn
 305 310 315 320
 Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg
 325 330 335
 Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr
 340 345 350
 Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly
 355 360 365
 Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala
 370 375 380
 Tyr Ile Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile
 385 390 395 400
 Ile Ala Ala Val Leu Phe Trp Gly Gly Gly Val Leu Leu Phe Ile Gln
 405 410 415
 Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu
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 Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr
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 Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr
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 465 470 475 480
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 485 490 495
 Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly
 500 505 510
 Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe
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<213> Homo sapiens

<220>

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<222> (147)..(1799)

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Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
 220 225 230
 gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt 893
 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
 235 240 245
 gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg 941
 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
 250 255 260 265
 ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc 989
 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
 270 275 280
 cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc 1037
 Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
 285 290 295
 caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt 1085
 Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
 300 305 310
 gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att 1133
 Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
 315 320 325
 ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct 1181
 Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
 330 335 340 345
 ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg 1229
 Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
 350 355 360
 gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct 1277
 Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
 365 370 375
 gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga 1325
 Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg
 380 385 390
 acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga 1373
 Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
 395 400 405
 ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta 1421
 Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
 410 415 420 425
 tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc 1469
 Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
 430 435 440
 tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg 1517
 Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg

A1

445 450 455
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 Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
 460 465 470
 att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc 1613
 Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
 475 480 485
 tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt 1661
 Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
 490 495 500 505
 ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag 1709
 Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
 510 515 520
 atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca 1757
 Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
 525 530 535
 atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc 1799
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 aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc 1919
 tatcaagaaa tgctcgtcac acagtaaact ctggatgatt cttccagata atgtccttgc 1979
 tttaaaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg 2039
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 35 40 45
 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
 50 55 60
 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His

A1

65 70 75
 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
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 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
 100 105 110
 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
 115 120 125
 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
 130 135 140
 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
 145 150 155
 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
 160 165 170 175
 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
 180 185 190
 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
 195 200 205
 Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
 210 215 220
 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
 225 230 235
 Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
 240 245 250 255
 Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
 260 265 270
 Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
 275 280 285
 Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
 290 295 300
 Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
 305 310 315
 Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
 320 325 330 335
 Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
 340 345 350
 Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
 355 360 365
 Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu

A1

370 375 380
 Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
 385 390 395
 Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
 400 405 410 415
 Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
 420 425 430
 Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
 435 440 445
 Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
 450 455 460
 Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
 465 470 475
 Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
 480 485 490 495
 Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
 500 505 510
 Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
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 <222> (124)..(1794)

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 ggc atg cgg gac tac gac gag gtg acc gcc ttc ctg ggc gag tgg ggg 168
 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly
 1 5 10 15
 ccc ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc 216
 Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro
 20 25 30

A1

aat ggc ttc acc ggc ctg tcc tcc gtg ttc ctg ata gcg acc ccg gag	264
Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu	
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cac cgc tgc cgg gtg ccg gac gcc gcg aac ctg agc agc gcc tgg cgc	312
His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg	
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aac cac act gtc cca ctg cgg ctg cgg gac ggc cgc gag gtg ccc cac	360
Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His	
65 70 75	
agc tgc cgc cgc tac cgg ctg gcc acc atc gcc aac ttc tcg gcg ctc	408
Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu	
80 85 90 95	
ggg ctg gag ccg ggg cgc gac gtg gac ctg ggg cag ctg gag cag gag	456
Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu	
100 105 110	
agc tgt ctg gat ggc tgg gag ttc agt cag gac gtc tac ctg tcc acc	504
Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr	
115 120 125	
att gtg acc gag tgg aac ctg gtg tgt gag gac gac tgg aag gcc cca	552
Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro	
130 135 140	
ctc aca atc tcc ttg ttc ttc gtg ggt gtg ctg ttg ggc tcc ttc att	600
Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile	
145 150 155	
tca ggg cag ctg tca gac agg ttt ggc cgg aag aat gtg ctg ttc gtg	648
Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val	
160 165 170 175	
acc atg ggc atg cag aca ggc ttc agc ttc ctg cag atc ttc tcg aag	696
Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys	
180 185 190	
aat ttt gag atg ttt gtc gtg ctg ttt gtc ctt gta ggc atg ggc cag	744
Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln	
195 200 205	
atc tcc aac tat gtg gca gca ttt gtc ctg ggg aca gaa att ctt ggc	792
Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly	
210 215 220	
aag tca gtt cgt ata ata ttc tct acg tta gga gtg tgc ata ttt tat	840
Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr	
225 230 235	
gca ttt ggc tac atg gtg ctg cca ctg ttt gct tac ttc atc cga gac	888
Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp	
240 245 250 255	
tgg cgg atg ctg ctg gtg gcg ctg acg atg ccg ggg gtg ctg tgc gtg	936

A1

Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
 260 265 270

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 Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
 275 280 285

gga cga ttt gaa gag gca gag gtg atc atc cgc aag gct gcc aaa gcc 1032
 Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
 290 295 300

aat ggg att gtt gtg cct tcc act atc ttt gac ccg agt gag tta caa 1080
 Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
 305 310 315

gac cta agt tcc aag aag cag cag tcc cac aac att ctg gat ctg ctt 1128
 Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
 320 325 330 335

A1 cga acc tgg aat atc cgg atg gtc acc atc atg tcc ata atg ctg tgg 1176
 Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
 340 345 350

atg acc ata tca gtg ggc tat ttt ggg ctt tcg ctt gat act cct aac 1224
 Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
 355 360 365

ttg cat ggg gac atc ttt gtg aac tgc ttc ctt tca gcg atg gtt gaa 1272
 Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu
 370 375 380

gtc cca gca tat gtg ttg gcc tgg ctg ctg ctg caa tat ttg ccc cgg 1320
 Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
 385 390 395

cgc tat tcc atg gcc act gcc ctc ttc ctg ggt ggc agt gtc ctt ctc 1368
 Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
 400 405 410 415

ttc atg cag ctg gta ccc cca gac ttg tat tat ttg gct aca gtc ctg 1416
 Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
 420 425 430

gtg atg gtg ggc aag ttt gga gtc acg gct gcc ttt tcc atg gtc tac 1464
 Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
 435 440 445

gtg tac aca gcc gag ctg tat ccc aca gtg gtg aga aac atg ggt gtg 1512
 Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
 450 455 460

gga gtc agc tcc aca gca tcc cgc ctg ggc agc atc ctg tct ccc tac 1560
 Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
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ttc gtt tac ctt ggt gcc tac gac cgc ttc ctg ccc tac att ctc atg 1608
 Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met

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Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu				
	500	505	510	
agc ttc ggt acc cca ctc cca gac acc att gac cag atg cta aga gtc				1704
Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val				
	515	520	525	
aaa gga atg aaa cac aga aaa act cca agt cac aca agg atg tta aaa				1752
Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys				
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A1
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 5
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<210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 6
 tgtagcgtga agacgacaga a 21

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 7
 tcgagcggcc gcccgggcag gt 22

<210> 8

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 8
 agggcggtggt gcggagggcg gt 22

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 9
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<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 10
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<210> 11
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 12
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 <213> Artificial Sequence

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<400> 12

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tcacacagga aacagctatg ac 22

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 13
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<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 14
 agctgcatga agagaaggac actg 24

<210> 15
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 15
 agcatcctgt ctccctactt cggt 24

<210> 16
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 <213> Artificial Sequence

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<210> 17
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 <212> DNA
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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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<213> Artificial Sequence

<220>
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<210> 20
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<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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aggcttttga tttgttctgt tgag 24

<210> 22
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A1

<212> PRT

<213> Mus musculus

<400> 22

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 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45
 Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
 50 55 60
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
 85 90 95
 Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
 115 120 125
 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
 130 135 140
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
 145 150 155 160
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
 165 170 175
 Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
 180 185 190
 Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
 195 200 205
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240
 Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
 260 265 270
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285

A1

Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
 385 390 395 400
 Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415
 Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
 420 425 430
 Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445
 Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460
 Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
 465 470 475 480
 Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
 500 505 510
 Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
 515 520 525
 Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
 530 535 540
 Ser Pro Lys Val Leu Ile Thr Ala Phe
 545 550

<210> 23

<211> 2083

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (122)..(1780)

<400> 23

attcggcaca ggacggcgtg tttgaacgagc cacctaggaa gatccccctca gcgcgccgaa 60

tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctgaggagga gaggtggaaa 120

c atg cgg gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc 169
Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
1 5 10 15

ttc cag cgc ctc atc ttc ttt ctg ctc agc gcc agc atc atc ccc aat 217
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
20 25 30

ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac 265
Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
35 40 45

cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac 313
Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
50 55 60

cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc 361
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg 409
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
85 90 95

ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc 457
Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc 505
Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
115 120 125

gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc 553
Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
130 135 140

acc acc tcc ctg ttc ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct 601
Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
145 150 155 160

ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc 649
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
165 170 175

atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac 697
Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
180 185 190

tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc 745

A1

Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
 195 200 205
 tcc aac tac gtg gtg gcc ttc ata cta gga act gaa atc ctg agc aag 793
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220
 tcg gtt cgc atc atc ttc tcc aca tta gga gtc tgt aca ttt ttt gca 841
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240
 atc ggc tac atg gtc ctg ccg ctg ttt gca tac ttc atc aga gac tgg 889
 Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 agg atg ctg ctg ctg gcc ctg aca ctg cct ggc ctg ttc tgt gtt ccc 937
 Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
 260 265 270
 ctg tgg tgg ttt att cca gaa tct ccc cgg tgg ctg ata tcc cag agg 985
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285
 aga ttt gca gag gcc gaa cag atc atc cag aaa gcc gca aag atg aac 1033
 Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 agc atc gtg gcg cca gca ggg ata ttc gat cct cta gag cta cag gag 1081
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320
 cta aac tcc ttg aag cag cag aaa gtc ata atc ctg gac ctg ttc agg 1129
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335
 act cgg aac att gcc acc ata acc gtg atg gct gtg atg ctg tgg atg 1177
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350
 cta acc tca gtg ggt tac ttt gct ctg tct ctc aat gtt cct aat tta 1225
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365
 cat gga gat gtc tac ctg aac tgc ttc ctc tct ggc ctg att gaa gtt 1273
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380
 cca gct tac ttc aca gcc tgg ctg cta ctg cga acc ctg cca cgg aga 1321
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
 385 390 395 400
 tat att ata gct ggg gtg cta ttc tgg gga gga ggt gtg ctt ctc ttg 1369
 Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415
 atc caa gtg gta cct gaa gat tat aac ttt gtg tcc att gga ctg gtg 1417
 Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val

A1

420	425	430	
atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc			1465
Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val			
435	440	445	
ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc			1513
Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly			
450	455	460	
atc acc tcc atg gcc tct cgg gtg ggc agc atc att gcc ccc tat ttc			1561
Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe			
465	470	475	480
gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc			1609
Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly			
485	490	495	
agt ctg act gtc ctc att gga atc atc acg ctt ttt ttc cct gaa agt			1657
Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser			
500	505	510	
ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga			1705
Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg			
515	520	525	
ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa			1753
Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu			
530	535	540	
agc ccc aag gtt cta ata act gca ttc taacgaggtt tccaaggcac			1800
Ser Pro Lys Val Leu Ile Thr Ala Phe			
545	550		
ttggcaaaact gaaaagcaga tgtatacaat gagcaggggtg tgatagagca agcctgcaat			1860
cccagcgctc ttgggggtgga gacagaagat caggagttca aggtcatcct tggctacagc			1920
aggagtgtaa gaccagcctg tcttaccaca agcaaccctg tctcaacaga acaaatacaa			1980
agccttttct gctgaaaggg attaacagaa acaatgagca ccaaactgga cttgtggaga			2040
aatgcacact atctcatgaa ttctgggcca ctcttcagaa tgg			2083
<210> 24			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence			
<400> 24			
cccattgcaa caaggacaaa aagc			24
<210> 25			

A1

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25
 acagaacaga aaagccctca gtca 24

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26
 tgtttttcgt ggggtgtgctg atgg 24

<210> 27
 <211> 557
 <212> PRT
 <213> Mus musculus

<400> 27
 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
 1 5 10 15
 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 20 25 30
 Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45
 Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95
 Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125
 Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser

41

145 150 155 160
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
 165 170 175
 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
 180 185 190
 Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
 195 200 205
 Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220
 Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240
 Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
 260 265 270
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285
 Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
 290 295 300
 Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320
 Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
 325 330 335
 Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
 340 345 350
 Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
 355 360 365
 His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
 370 375 380
 Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg
 385 390 395 400
 Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
 405 410 415
 Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
 420 425 430
 Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
 435 440 445
 Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly

A1

450 455 460
 Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
 465 470 475 480
 Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
 500 505 510
 Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
 515 520 525
 Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
 530 535 540
 Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
 545 550 555

<210> 28
 <211> 1888
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (60)..(1730)

<400> 28
 ctcccgcgcc acggtgtccc cttattccca tacgggcgct gtgggaggct gaggacggc 59

atg cgg gac tac gac gag gtg acc gcc ttc cta ggc gag tgg ggg ccc 107
 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
 1 5 10 15

ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc aat 155
 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 20 25 30

ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac 203
 Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45

cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac 251
 Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60

cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa 299
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg 347
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95

ctg gag ccg ggg cgg gac gtg gac ctg gag cag ctg gag cag gag agc 395

41

Leu	Glu	Pro	Gly	Arg	Asp	Val	Asp	Leu	Glu	Gln	Leu	Glu	Gln	Glu	Ser	
			100					105						110		
tgc	ctg	gat	ggc	tgg	gag	tac	gac	aag	gac	gtc	ttc	ctg	tcc	acc	atc	443
Cys	Leu	Asp	Gly	Trp	Glu	Tyr	Asp	Lys	Asp	Val	Phe	Leu	Ser	Thr	Ile	
		115					120					125				
gtg	aca	gag	tgg	gac	ctg	gtg	tgt	aag	gat	gac	tgg	aaa	gcc	cca	ctc	491
Val	Thr	Glu	Trp	Asp	Leu	Val	Cys	Lys	Asp	Asp	Trp	Lys	Ala	Pro	Leu	
	130					135					140					
acc	acc	tcc	ttg	ttt	ttc	gtg	ggg	gtg	ctg	atg	ggc	tcc	ttc	att	tca	539
Thr	Thr	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Met	Gly	Ser	Phe	Ile	Ser	
145					150					155					160	
gga	cag	ctc	tca	gac	agg	ttt	ggg	cgc	aag	aat	gtg	ctg	ttt	ttg	acc	587
Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Asn	Val	Leu	Phe	Leu	Thr	
			165					170						175		
atg	ggc	atg	cag	act	ggc	ttc	agc	ttc	ctg	cag	gtc	ttc	tct	gtg	aac	635
Met	Gly	Met	Gln	Thr	Gly	Phe	Ser	Phe	Leu	Gln	Val	Phe	Ser	Val	Asn	
			180				185						190			
ttc	gag	atg	ttt	aca	gtg	ctt	ttt	gtc	ctt	gtt	ggc	atg	ggg	cag	atc	683
Phe	Glu	Met	Phe	Thr	Val	Leu	Phe	Val	Leu	Val	Gly	Met	Gly	Gln	Ile	
	195					200					205					
tcc	aac	tac	gtg	gca	gca	ttt	gtc	ctg	gga	aca	gaa	att	ctt	tcc	aag	731
Ser	Asn	Tyr	Val	Ala	Ala	Phe	Val	Leu	Gly	Thr	Glu	Ile	Leu	Ser	Lys	
	210					215					220					
tca	att	cga	att	ata	ttc	gcc	acc	tta	gga	gtt	tgc	ata	ttt	tat	gcg	779
Ser	Ile	Arg	Ile	Ile	Phe	Ala	Thr	Leu	Gly	Val	Cys	Ile	Phe	Tyr	Ala	
225					230				235					240		
ttt	ggc	ttc	atg	gtg	ctg	cca	ctg	ttt	gca	tac	ttc	atc	aga	gac	tgg	827
Phe	Gly	Phe	Met	Val	Leu	Pro	Leu	Phe	Ala	Tyr	Phe	Ile	Arg	Asp	Trp	
			245					250					255			
agg	atg	ctg	ctg	ctg	gcg	ctc	act	gtg	cca	ggg	gtg	cta	tgt	ggg	gct	875
Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Val	Pro	Gly	Val	Leu	Cys	Gly	Ala	
		260					265					270				
ctc	tgg	tgg	ttc	atc	cct	gag	tcc	cca	cga	tgg	ctc	atc	tct	caa	ggc	923
Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp	Leu	Ile	Ser	Gln	Gly	
	275					280					285					
cga	att	aaa	gag	gca	gag	gtg	atc	atc	cgc	aaa	gct	gcc	aaa	atc	aat	971
Arg	Ile	Lys	Glu	Ala	Glu	Val	Ile	Ile	Arg	Lys	Ala	Ala	Lys	Ile	Asn	
	290					295					300					
ggg	att	gtt	gca	cct	tcc	act	atc	ttc	gat	cca	agt	gag	tta	caa	gac	1019
Gly	Ile	Val	Ala	Pro	Ser	Thr	Ile	Phe	Asp	Pro	Ser	Glu	Leu	Gln	Asp	
305				310					315					320		
tta	aat	tct	acg	aag	cct	cag	ttg	cac	cac	att	tat	gat	ctg	atc	cga	1067
Leu	Asn	Ser	Thr	Lys	Pro	Gln	Leu	His	His	Ile	Tyr	Asp	Leu	Ile	Arg	

A1

	325	330	335	
	aca cgg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg			1115
	Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu			
	340	345	350	
	acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg			1163
	Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu			
	355	360	365	
	cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc			1211
	His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val			
	370	375	380	
	cca gcc tat gtg ctg gcc tgg ctg ttg ttg cag tac ttg ccc cgg cga			1259
	Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg			
	385	390	395	400
	tat tct atc tcg gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc			1307
	Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe			
	405	410	415	
41	atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg			1355
	Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val			
	420	425	430	
	atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg			1403
	Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val			
	435	440	445	
	tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg			1451
	Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly			
	450	455	460	
	gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt			1499
	Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe			
	465	470	475	480
	gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga			1547
	Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly			
	485	490	495	
	agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc			1595
	Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser			
	500	505	510	
	ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa			1643
	Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys			
	515	520	525	
	gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat			1691
	Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp			
	530	535	540	
	ggt gaa gaa agc cca aca gtc cta aag agc aca gcc ttc taacaccctg			1740
	Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe			
	545	550	555	

tccagaaggc aaaaaactga ttggaaacct tcatgttgctc agaaatgctc tccatgactg 1800
 agggcttttc tgttctgtta accttgtgctc taacatgctc atggattggg gcatctgtcc 1860
 tggagagtca ccttcctcta gggacacc 1888

<210> 29
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 29
 ctaatacgac tcactatagg gctcgagcgg ccgcccgggc aggt 44

<210> 30
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 30
 tgtagcgtga agacgacaga aagggcgtgg tgcggagggc ggt 43

<210> 31
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 31
 acctgcccgg 10

<210> 32
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 32
 accgccctcc g 11

A7